

Figure 1

A



wild type

sev-wg

sev-wg, $lgs^{S17}/+$

B



C

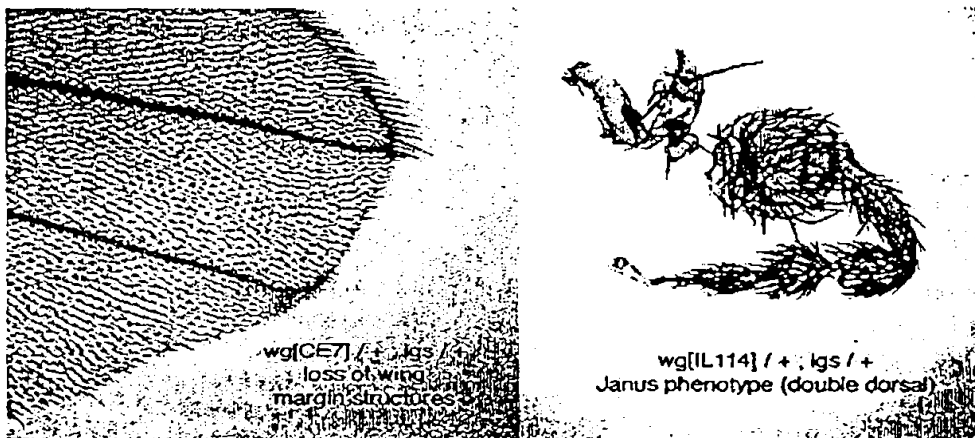


Figure 2

[illegible][illegible]

Figure 2: *logless*

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T N P P C A S N S I N F F Q M C M O N S 1252
ATTGTGACGACAGAGGTTGATTAACCCGCGCAACAGGATCAATGATATTCGTCAACCA 5860
I V D N E G C L P O M D C S N N I G O F 1272
TCTATGTAAGAGGCGCAATGCTCCACATGCGCAAGCGGCGCAATGATTAATGCGCGCGGATG 5940
S N I R G N A P R A N N P P V M G A N N 1292
CGAGGCGGTAAACAGCGCAATTCGATTTGCAAGTCAATGCAATGATGATGATGATGATGATG 6000
P P V N S Q I O F A G S S D O I D C V O 1312
CATGCGTCAATCTCTTCTAAGCTTCTGCGCAAGCGCTGCGCAAGCGCTCTCTTCTGCA 6060
D P S E T V T N A S C N S A S V N N T C 1332
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S A Q Q A N D P K T Q N E N N I P S O N 1352
TGTCAAAAGCAATCTGCGCTTCTGATGCGCAAGCGGCGCAATGCGCAATGCGCAATGCGCA 6180
C Q N O S C L A V A G S O I Q L N S Q G 1372
CATGCGCAGCGGCAATCTCTAATGCGCTTCTAATGCGCTTCTAATGCGCTTCTAATGCGCT 6240
N A Q C G U E L I O P T N N N L N S T A C 1392
AGTGTCAATCTCTGCAAGCGTCTCTGCGCAATCTCTGCGCAATCTCTGCGCAATCTCTGCG 6300
S V S A T M G C V S S I P P V O P S E T O 1412
CTCAAGTATGCGCGCAATCTCTAATGCGCTTCTGCGCAAGCGCTTCTGCGCAAGCGCTTCT 6360
L E X A Q O V N P P Q Q L V A T N T R 1432
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S Q Q O O N N D Q N G S N N I T N P P 1452
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N L E S D N V T P V N X 1465
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Figure 3

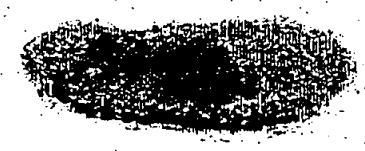
A



yw x lgs anti-sense



yw x lgs sense



B

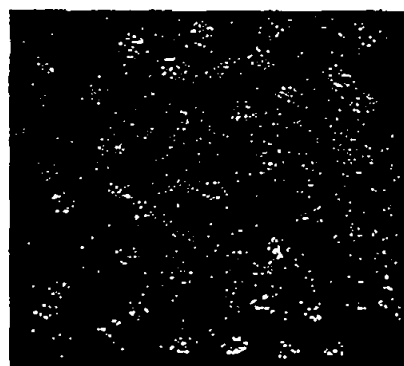
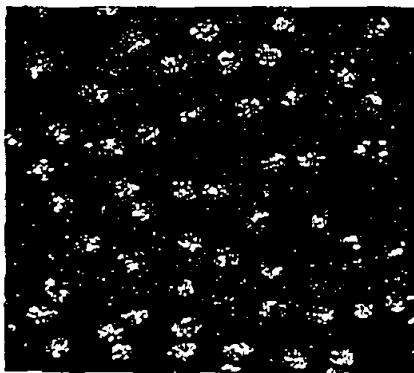


Figure 4

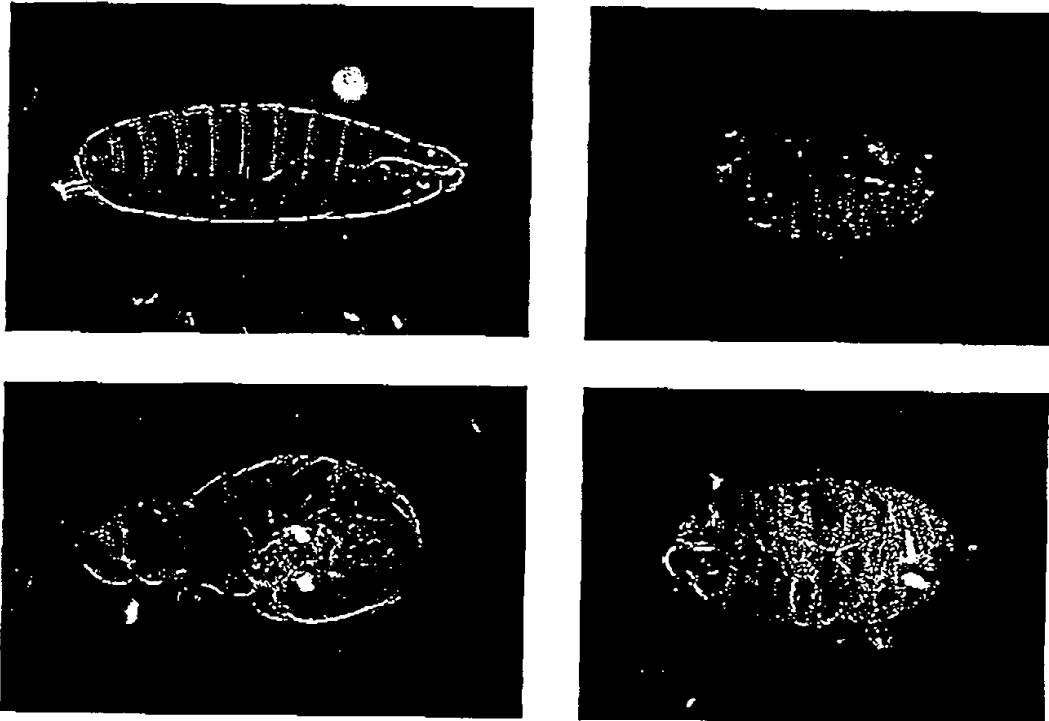
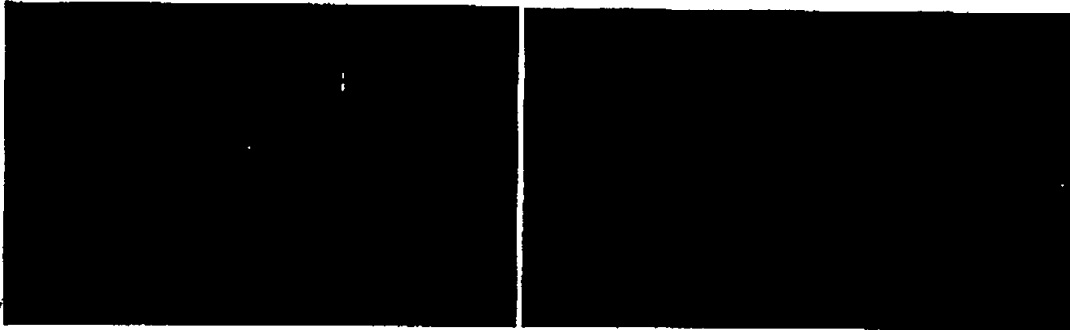


Figure 5

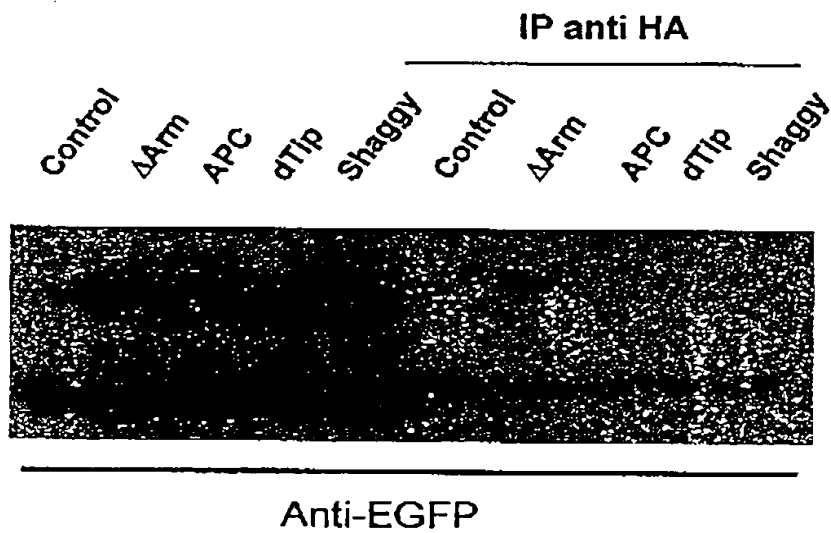
A

EGFP-Lgs

EGFP-Lgs + pcDNA3-Arm-NLS



B

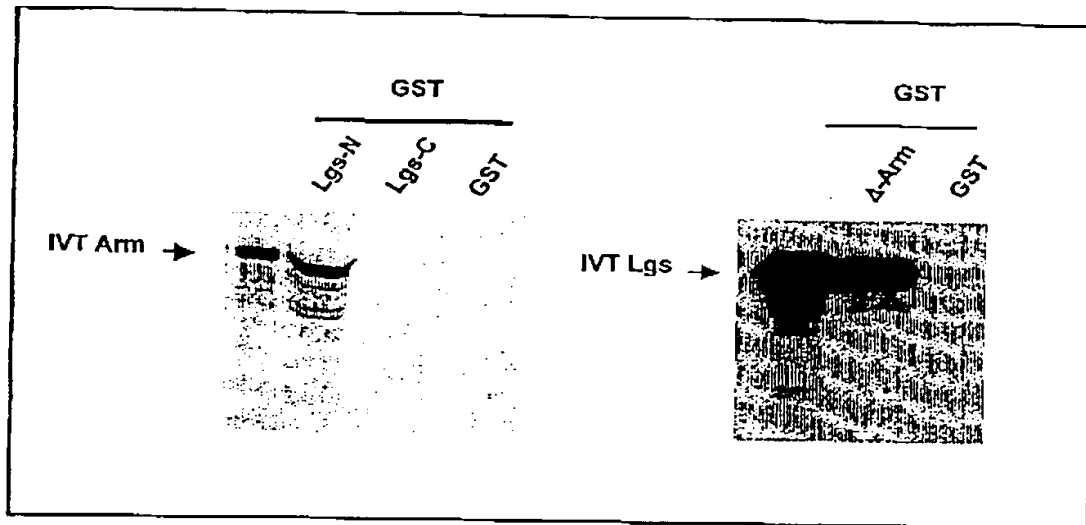


5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	Δ ArmC	Δ B-Cat	Pan
PREY fusions: pJG4-5	lgs364-655							
	lgs1-385							
	lgs1-732							
	lgs364-1090							
	lgs726-1464							
	lgs1-1464							
	BCL9 199-392							
	BCL9 1-1426							
	Dco+							
	Δ ArmC							
	B-Cat							
	Pan							
	pJG4-5							

+: interaction seen in yeast two-hybrid assay
 -: no interaction seen in yeast two-hybrid assay
 n.d.: not done
 numberings refer to amino acid positions.

5D



5E

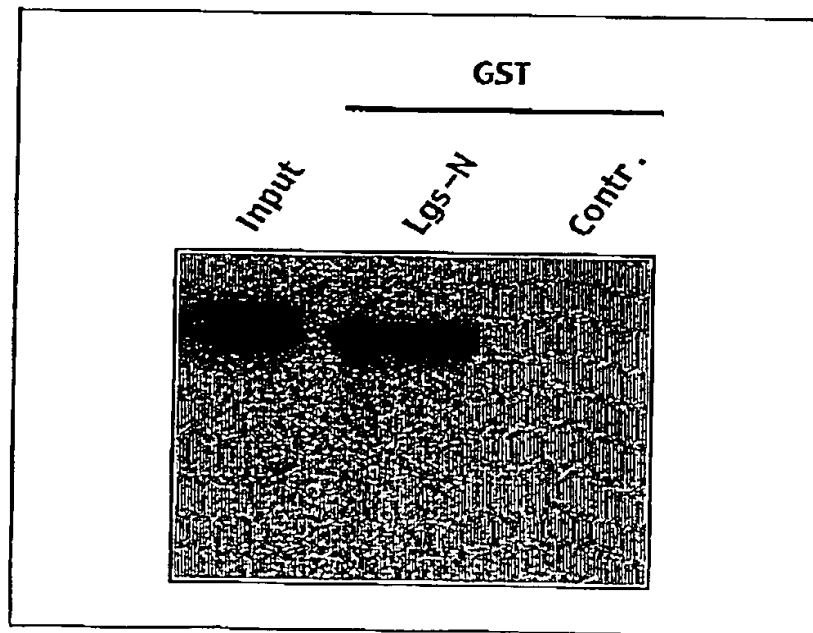


Figure 6

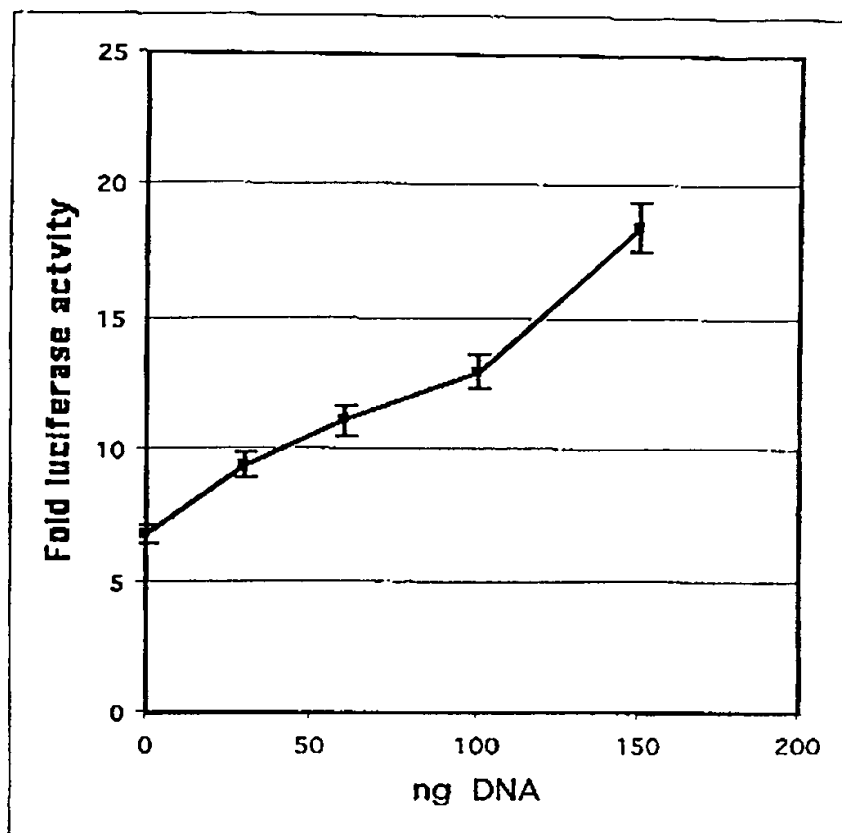
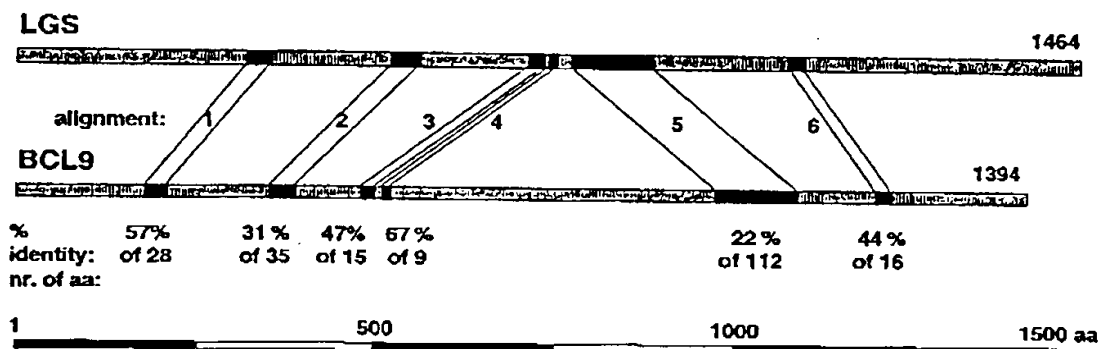


Figure 7

A



7B

Sequence homology domain 1: 57.1% identity in 28 aa

	320	330	340
LGS	IFVFSTQLANKGAESVLSGQFQTTIAYH		

BCL9	VYVFSTEMANKAAEAVALKGQVETIVSFH		
	180	190	200

Sequence homology domain 2: 31.4% identity in 35 aa

	520	530	540
LGS	ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA		

BCL9	DGLSQEQLEHRERSLQTLRDIOFMILFPDEKEFTGA		
	350	360	370 380

Sequence homology domain 3: 46.7% identity in 15 aa

	710	720
LGS	QMEWSKIQHQPFER	

BCL9	QIANLKLQEQFYEEK	
	470	480

Sequence homology domain 4: 66.6% identity in 9 aa

	760
LGS	LQGPPPPYH

BCL9	VRGPPPPYQ
	520

Sequence homology domain 5: 22.3% identity in 112 aa

	770	780	790	800	810	820
LGS	SASVPIATQSPNPFSSFNLSLPSPTTAAMMELPTNSPSMDGTGSLSGSVQANTSTVQA					

BCL9	GPPPTASQPASVNIPLSLPSSTFYTMPPEPTLSQNLPLSIM-MSRMSKFAMPSSTPLYHD					
	970	980	990	1000	1010	1020
	830	840	850	860	870	
LGS	GTTIVLSANKNCFQADTPSPSNQNRSRNIGSSSVLTHNLSSNPFSTPLSHLSP					

BCL9	AIKTVASSDDSPPARSPNLPSMNNMPGMGINTQNPRIISGPNFVVPMTLSP					
	1030	1040	1050	1060	1070	

Sequence homology domain 6: 43.8% identity in 16 aa

	1080
LGS	NPRMCVAGGPNPGPF

BCL9	DAALCKPGPGGPDSP
	1190 1200

Figure 8

A

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GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCOOOCTACAGTGA
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TCCCACAACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG
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GCCCTCTGAGTCTTCTAGGGGTGACTTTCCAAAAGGAATCCOCCACAG

Figure 8A

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GCTCTACACCCACCCCTGGGCTGTGGGCTCTCCAGGCATGATGATGTCCA
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCAGAGATG
AGGCCCCGGGGCATGGCTGCTGACGTGGGCATGGGTGGATTTAGCCAAGG
ACCTGGCAACCCAGGAAACATGATGTTTTAA

Figure 8B

B

MHSSNPKVRSSPSGNTQSSPKSKQEVMMVRPPTVMSPSGNPQLDSKFSNOG
KQGGASASQSQSPCDKSKGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE
RSISADSFQQRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA
PRSSTPSHGOTTATEPTPAQKTPAKVVVFSTEMANKAAEAVLKGOVETI
VSFHQINISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ
NTRLQPTTPIAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP
DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG
LSQEQLHFRERSLQTLRDIQRMILFPDEKEFTGAQSGGPOQNPQVLDGPQK
KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPOGHRDVPFSPDEM/PPSM
NSQSGTIGPDHLDHMTPEQIAWLKQQEFYEEKRRKQEQVWVQQCSLQDM
MVHQHGPRGVVRGPPPPYQMTPEGWAPGGTEPFSDGINMPHSLPPRGMA
PHPNMIPGSMPLPGFAGMINSEMEGPNVNPASRPLSGVSWPDDVPKIP
DGRNFPFGQIFSGPGRGERFPNPOGLSEEMFQQQLAEKQLGLPPGMAME
GIRPSMEMNRMIPGSRHIMEPGNINPIFPIPVVEGPLSPSRGDFPKGIPPQ
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RPGGSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPSSNSGLRNL
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VFPFHNGPSGGQGSFPGGMGFPGEGLGRPSNLQSSADAALCKPGGPGG
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Figure 9

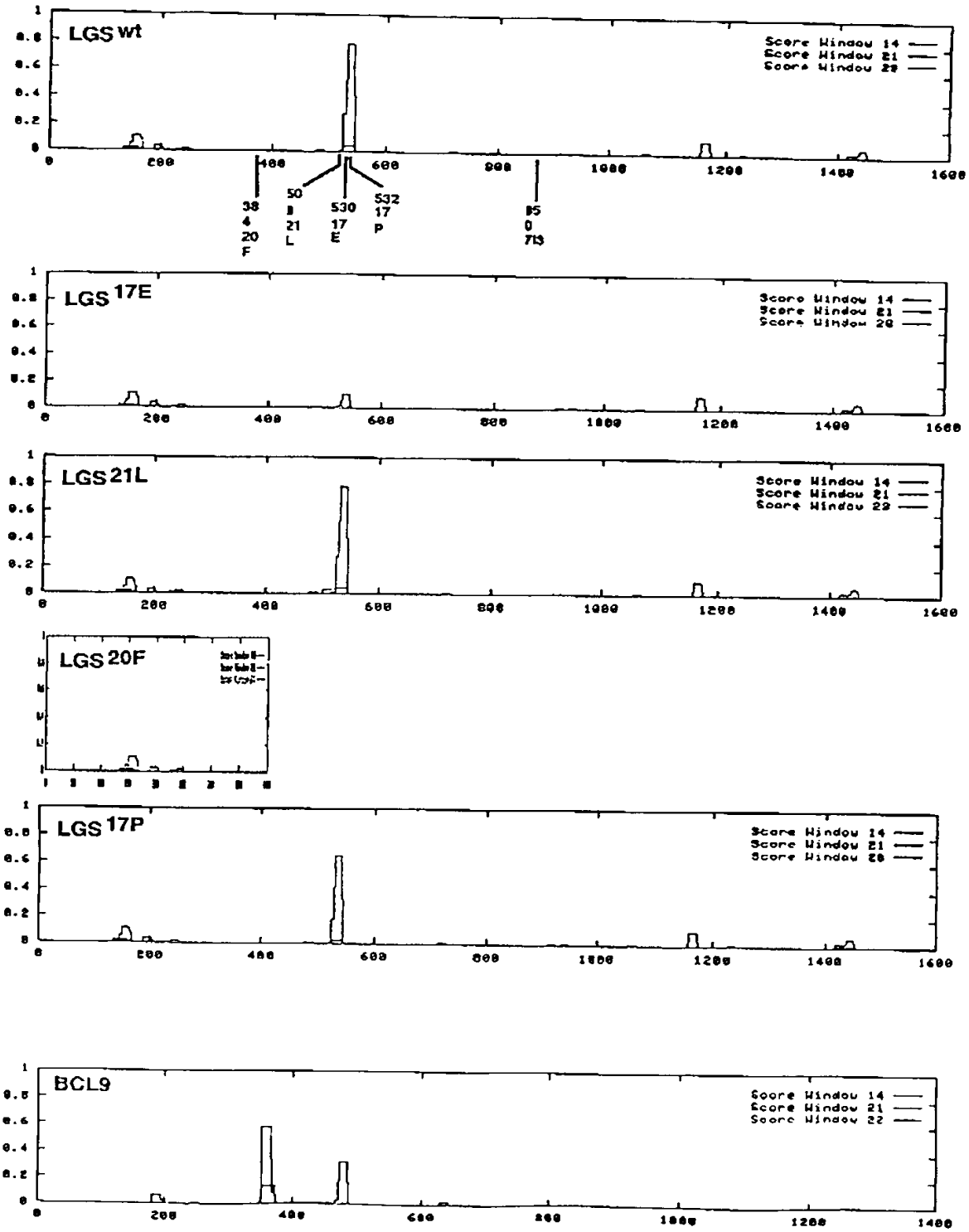


Figure 10

A

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Figure 10

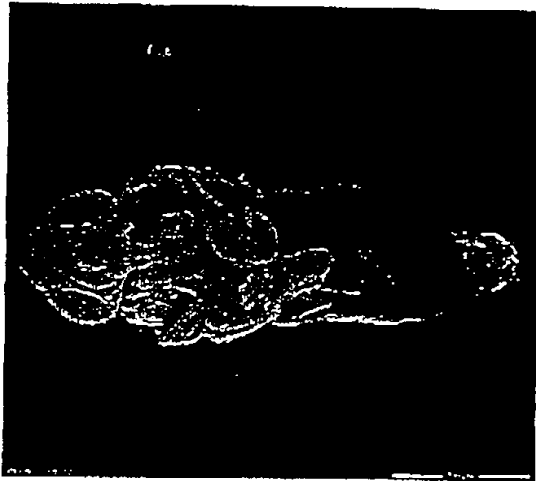
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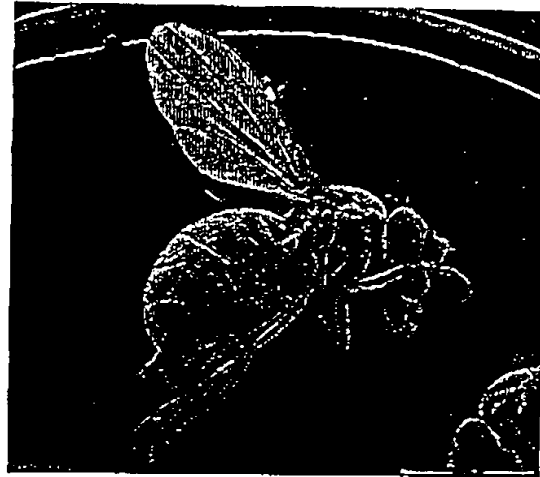
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PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLEKRSMMGMQR
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GGRGLSPPMGQSGLEVDPPMGPGNLNMINMNMNMNMNMNLNVQMT PQQQ
MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP
QVLGSSLSVRSPTGSPSRKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP
PLNMNSSTTLNMEQDPTPSQNPLSLMMTQMSKYAMPSSSTPLYHNAIKTI
ATSDDELLPDRPLLPPPPPPQSGSGPGGDSLNAPOGPVPSSSQMMPFPPR
LQQPHGAMAPTGGGGGGPGGLQCHYPSGMALPPEDLPNQPPGPMPPQQHLM
GKAMAGRMGDAYPPGVLPGVASVLNDPELSEVIRPTPTGIPEFDLSRIIP
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPQQQ
GDRPLVWIFGTRAMAPAQRCP LCRQTFFCGRGHVYSRIKHQRQLKEALER
LLPQVEAARKAIRAAQVERYVPEHERCCWQLOCGCEVREHLSHGNTVLY
GGLLEHLASPEHKATNKFWWENKAEVQMKELVTPQDYARFKKSMVKG
LDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV
LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPTH
TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD
DTVLGVKLSIANYDL

Figure 11

A



B



A

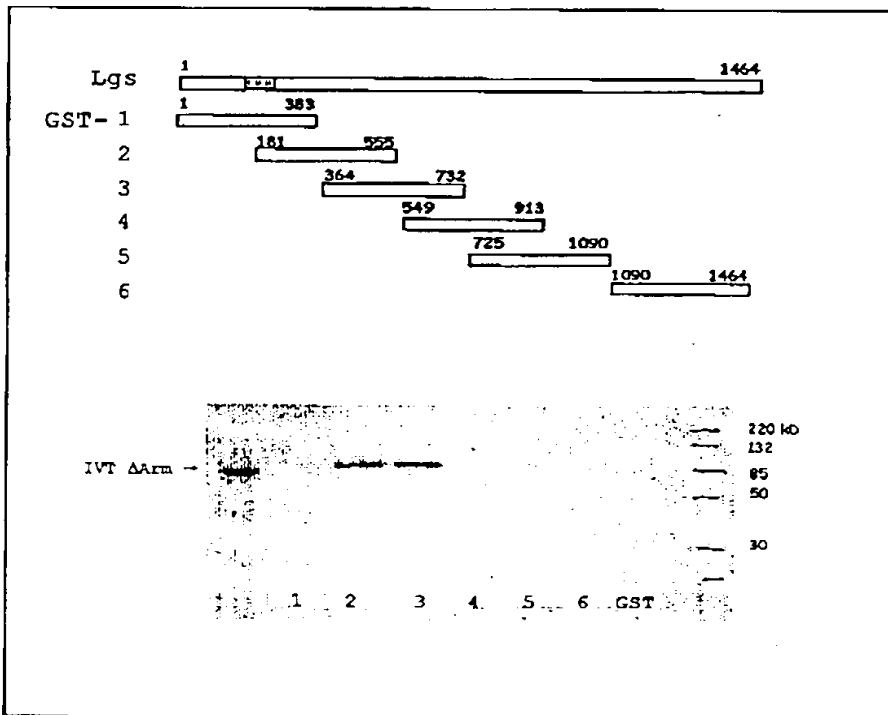


Figure 12B

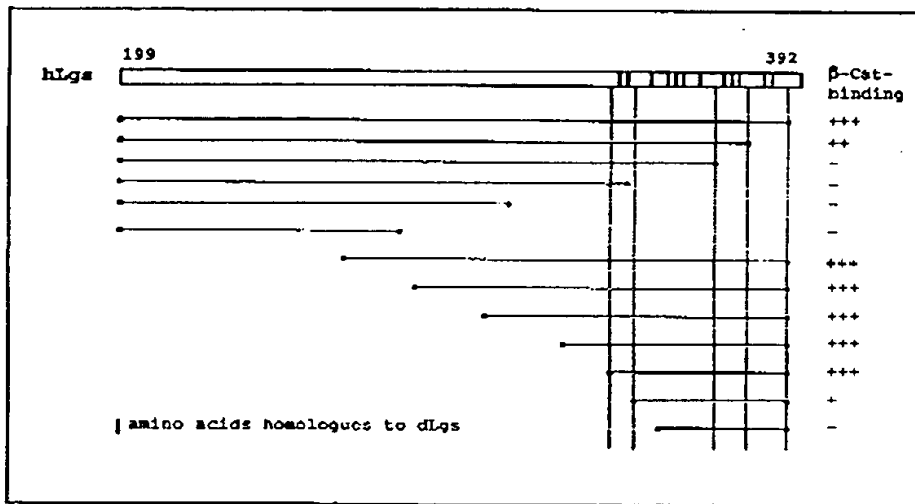
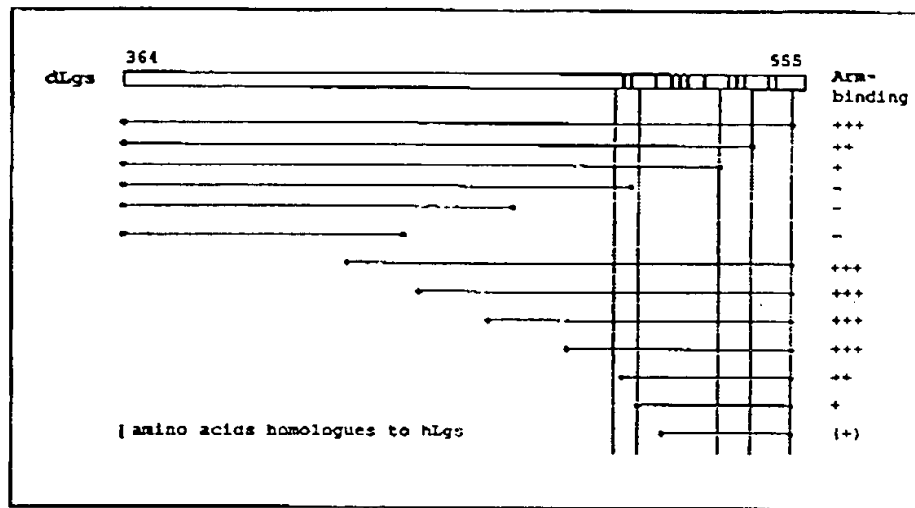


Figure 12C



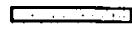





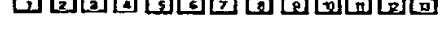
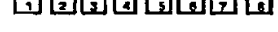

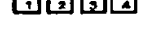

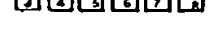

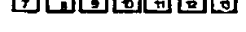

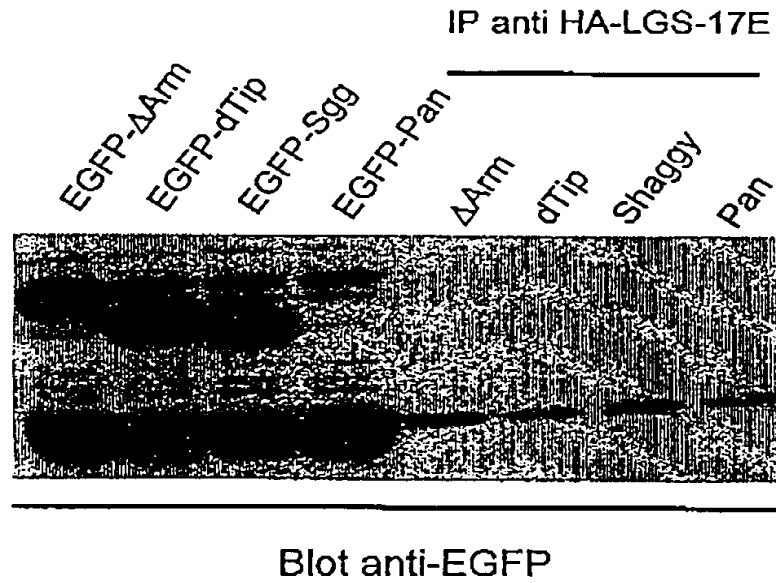
	In vitro interaction
N  C	++
 C	++
 C	-
N  C	++
N  C	+++
N  C	+++
N  C	++
N  C	-
 C	++
 C	+++
 C	+++
 C	++
 C	-
 C	(+)
 C	(-)
 C	(-)
 C	(-)

Figure 13

A



B

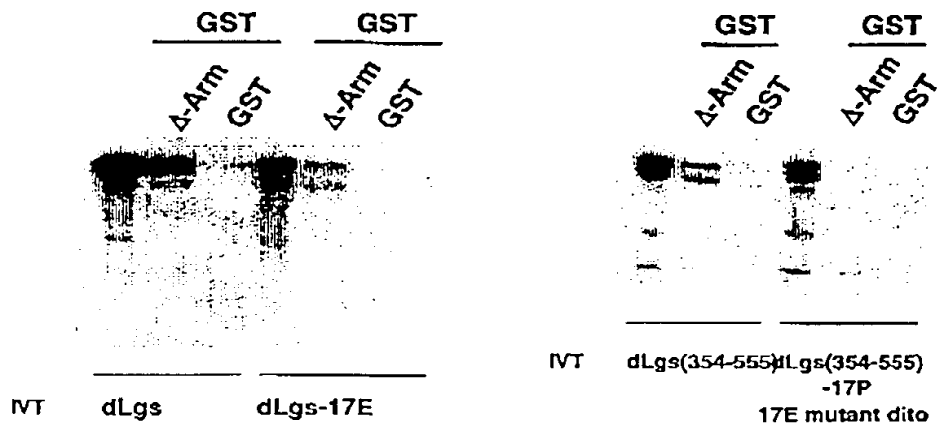
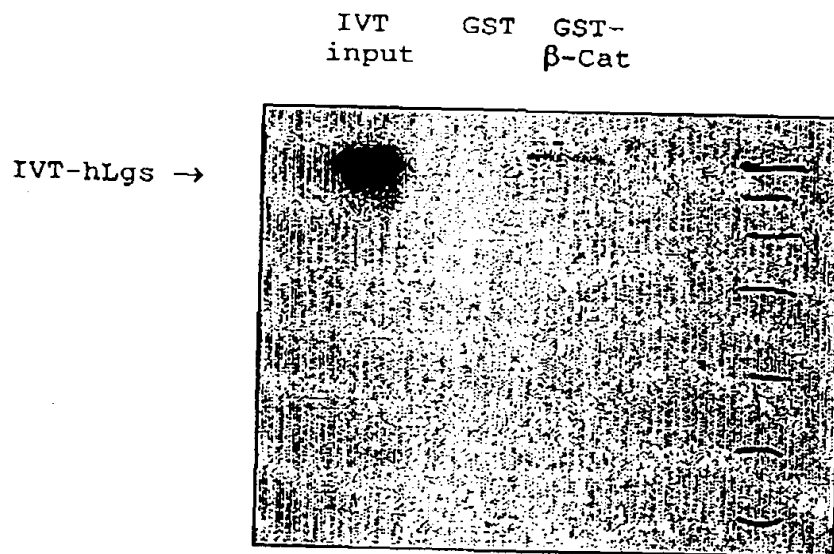


Figure 13

C



D

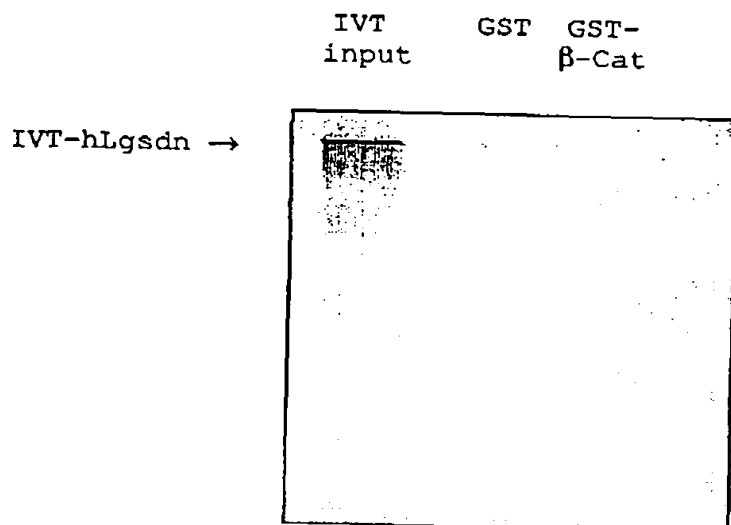
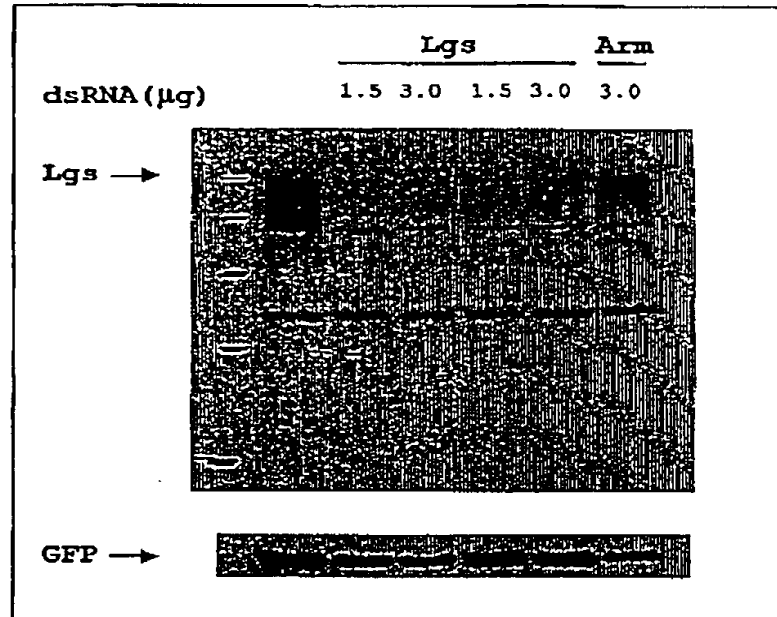
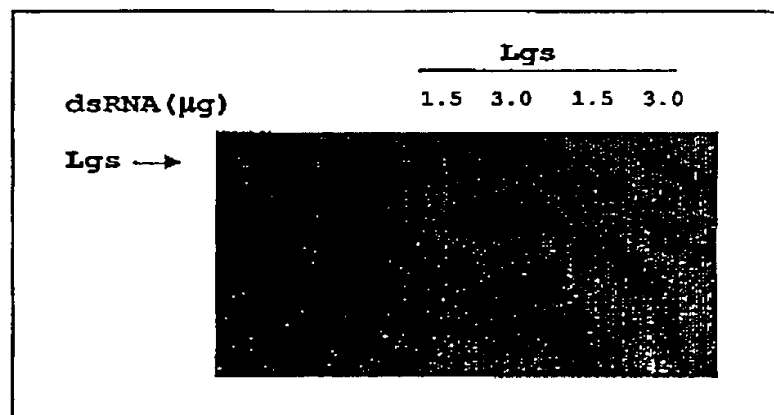


Figure 14



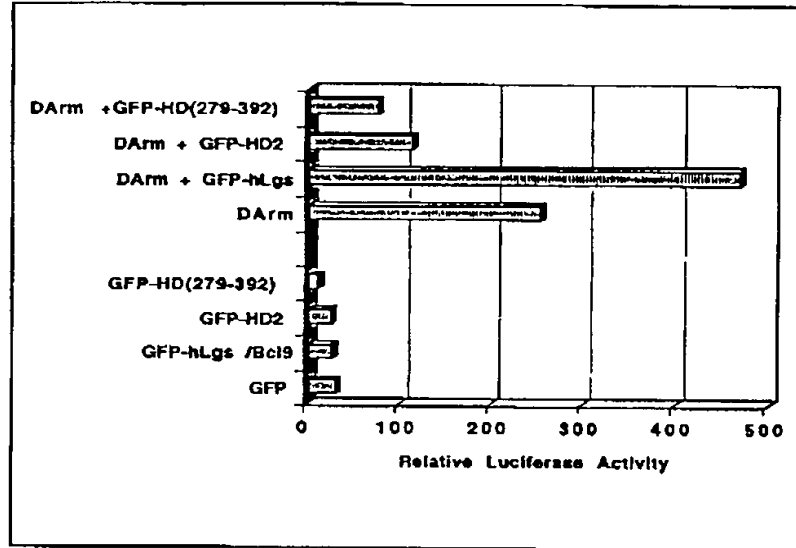
pMT-EGFP (μ g) 1.5 1.5 1.5 1.5 1.5 1.5



pMT-dLgs (μ g) - 2 2 2 2 2

Figure 15

A



B

